Docket No: 38-10(15486)B

Amended Claims

1. A method for analyzing mRNA in select eukaryotic cells comprising

(a) pausing transcription in the nuclei of select eukaryotic cells containing nascent mRNA transcripts,

(b) incubating said nuclei with labeled nucleoside triphosphate to produce labeled RNA molecules from said nascent mRNA transcripts,

A1 (c) contacting said labeled RNA molecules with an array of at least 500 nucleic acid molecule probes representing at least part of the genome of the native eukaryotic organism for said cells to identify the quantity of nascent mRNA transcripts in said cells and

(d) determining a transcription rate for at least one of said mRNA transcripts.

8. A method for analyzing mRNA molecules in a eukaryotic cell, said method comprising

(a) pausing transcription in select eukaryotic cells containing nuclei with nascent mRNA transcripts,

A2 (b) using labeled mRNA transcripts to show a relative rate of synthesis for a plurality of mRNA molecules, and

(c) determining a frequency of synthesis for a plurality of said mRNA transcripts.

9. A method according to claim 8 further comprising the steps of:

(d) using at least part of said cells to determine a steady-state level of mRNA at the time of said pausing; and

(e) determining relative rates of mRNA degradation for mRNA transcripts by comparing frequencies of synthesis and steady-state concentrations.

Docket No: 38-10(15486)B

Marked Up Version of Amended Claims

1. A method for [determining transcription rate of] analyzing mRNA in select eukaryotic cells comprising

(d) pausing transcription in the nuclei of select eukaryotic cells containing nascent mRNA transcripts,

(e) incubating said nuclei with labeled nucleoside triphosphate to produce labeled RNA molecules from said nascent mRNA transcripts,

(f) contacting said labeled RNA molecules with an array of at least 500 nucleic acid molecule probes representing at least part of the genome of the native eukaryotic organism for said cells to identify the quantity of nascent mRNA transcripts in said cells and

(d) determining a transcription rate for at least one of said mRNA transcripts.

8

10. A method for [~~determining a frequency of synthesis for a plurality of~~] analyzing mRNA molecules in a eukaryotic cell, said method comprising

(a) pausing transcription in select eukaryotic cells containing nuclei with nascent mRNA transcripts, [and]

(b) using labeled mRNA transcripts to show a relative rate of synthesis for a plurality of mRNA molecules, and

(c) determining a frequency of synthesis for a plurality of said mRNA transcripts.

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9

11. A method according to claim 8 [for determining a rate of degradation for a distinct mRNA molecule in a eukaryotic cell, said method] further comprising the steps of:

[(c) pausing transcription of mRNA in select eukaryotic cells containing nuclei with nascent mRNA transcripts,

(d) using at least part of said nuclei to determine a frequency of synthesis for a plurality of mRNA transcripts at the time of said pausing:

(e)] (d) using at least part of said cells to determine a steady-state level of mRNA at the time of said pausing; and

[(f)] (e) determining relative rates of mRNA degradation for mRNA transcripts by comparing frequencies of synthesis and steady-state concentrations.

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FACSIMILE

نسخة طبق الأصل

ファクシミリ送付状

FAC-SIMILÉ

Факсимиле

FAKSIMILE

फैक्समिलि

TELEFAX

โทรสาร

FAC-SÍMILE

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TELEFAKS

전송 사진

FAKSYMILE

传真

FAX

DATE	September 19, 2002
TO	Assistant Commissioner for Patents Attn: Examiner Ethan C. Whisenant Art Unit: 1634
FAX	703-308-4242
FROM	Thomas E. Kelley
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CC	
SUBJECT	Corrected Marked-Up Version of Amended Claims
PAGES	3 including this cover sheet

In re: Application of Thomas P. Beals
Serial No. 09/955,869
Filed: 09/19/2001
For: Methods for gene array analysis of nuclear runoff transcripts
Docket No. 38-10(15486)B

A response to Restriction Requirement and Preliminary Election was faxed to the USPTO on September 18, 2002 with typographical errors in the marked-up version of amended claims, e.g. claims 8 and 9 are misnumbered, in claim 1 the subparagraphs are misnumbered and in claim 8 deleted words are struck through. The enclosed two sheets are a corrected marked-up version of the amended claims. Applicant regrets any inconvenience in the examination of this application caused by this error.

Respectfully submitted,

Thomas E. Kelley
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Marked Up Version of Amended Claims

1. A method for [determining transcription rate of] analyzing mRNA in select eukaryotic cells comprising

(a) pausing transcription in the nuclei of select eukaryotic cells containing nascent mRNA transcripts,

(b) incubating said nuclei with labeled nucleoside triphosphate to produce labeled RNA molecules from said nascent mRNA transcripts,

(c) contacting said labeled RNA molecules with an array of at least 500 nucleic acid molecule probes representing at least part of the genome of the native eukaryotic organism for said cells to identify the quantity of nascent mRNA transcripts in said cells and

(d) determining a transcription rate for at least one of said mRNA transcripts.

8. A method for [determining a frequency of synthesis for a plurality of] analyzing mRNA molecules in a eukaryotic cell, said method comprising

(a) pausing transcription in select eukaryotic cells containing nuclei with nascent mRNA transcripts, [and]

(b) using labeled mRNA transcripts to show a relative rate of synthesis for a plurality of mRNA molecules, and

(c) determining a frequency of synthesis for a plurality of said mRNA transcripts.

9. A method according to claim 8 [for determining a rate of degradation for a distinct mRNA molecule in a eukaryotic cell, said method] further comprising the steps of:

[(c) pausing transcription of mRNA in select eukaryotic cells containing nuclei with nascent mRNA transcripts,

(d) using at least part of said nuclei to determine a frequency of synthesis for a plurality of mRNA transcripts at the time of said pausing:

(e)] (d) using at least part of said cells to determine a steady-state level of mRNA at the time of said pausing; and

[(f)] (e) determining relative rates of mRNA degradation for mRNA transcripts by comparing frequencies of synthesis and steady-state concentrations.